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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=29; hr=12; min=6; sec=8; ms=469;]

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Reviewer Comments:

<210> 18

<211> 33

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<220>

<221> misc_feature

<222> (22)..(24)

<223> The residues in these positions could be any amino acid

<400> 18

agggccagtc agttcgttgg cnnagcatc cac

33

The above <223> response explaining the "n's" at locations 22-24 is incorrect. This is not an amino acid sequence; it is a nucleotide sequence. Same error in Sequences 24, 30, 32, 42, 48, and 52 (and possibly in subsequent sequences).

Application No: 10541260

Version No: 2.0

Input Set:**Output Set:****Started:** 2007-11-09 11:44:33.311**Finished:** 2007-11-09 11:44:35.401**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 90 ms**Total Warnings:** 104**Total Errors:** 0**No. of SeqIDs Defined:** 122**Actual SeqID Count:** 122

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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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Input Set:

Output Set:

Started: 2007-11-09 11:44:33.311
Finished: 2007-11-09 11:44:35.401
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 90 ms
Total Warnings: 104
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Watkins, Jeffry D.
Vasserot, Alain P.
Marquis , David
Huse , William D.

<120> TNF-alpha Binding Molecules

<130> X-16758M

<140> 10541260

<141> 2005-06-30

<150> PCT/US04/00290

<151> 2004-01-08

<150> 10/338,552

<151> 2003-01-08

<150> 10/338,627

<151> 2003-01-08

<160> 122

<170> PatentIn version 3.3

<210> 1

<211> 107

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 1

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1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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gatcagtcctc caaagctcct catcaagtat gcttctgagt ctatgtctgg ggtcccctcg 180
aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240
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gggaccaagg tggaaatcaa a 321

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<211> 120
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 3

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser

65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 4
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<213> Artificial

<220>
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ccaggaaggg ggctggagtg ggttggcgaa attagatcaa aatctattaa ttctgcaaca 180
cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca 240
ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300
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<210> 5
<211> 107
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<220>
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<400> 5

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Tyr Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 6

<211> 321

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<220>

<223> Synthetic Construct

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gatcagtcctc caaagctcct catcaagtat gcttctgagt ctaggtctgg ggtcccctcg 180

aggttcagtg gcagtggatc tgggacagat ttcacctca ccatcaatag cctggaagct 240

gaagatgctg ccacgtatta ctgtcaacaa agtcatagct ggcatttcac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 7

<211> 120

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 7

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 8
<211> 360
<212> DNA
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<220>
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ccaggaaggg ggctggagtg ggttggcgaa attagatcaa aatctatgaa ttctgcaaca 180
cattatgcgg agtctgtgaa aggagattc accatctcaa gagatgattc aaagaactca 240
ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300
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<210> 9
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 9

Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His
1 5 10

<210> 10
<211> 33
<212> DNA
<213> Artificial

<220>
<223> Synthetic Construct

<400> 10
agggccagtc agttcggttg ctcaagcatc cac 33

<210> 11
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 11

Arg Ala Ser Gln Phe Val Gly Leu Ser Ile His
1 5 10

<210> 12
<211> 33
<212> DNA
<213> Artificial

<220>
<223> Synthetic Construct

<400> 12
agggccagtc agttcggttg ccttagcatc cac 33

<210> 13
<211> 11
<212> PRT
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<220>
<223> Synthetic Construct

<400> 13

Arg Ala Ser Gln Phe Val Gly Met Ser Ile His
1 5 10

<210> 14

<211> 33
 <212> DNA
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 <400> 14
 agggccagtc agttcgttgg catgagcatc cac 33

<210> 15
 <211> 11
 <212> PRT
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 <220>
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<400> 15

 Arg Ala Ser Gln Phe Val Gly Tyr Ser Ile His
 1 5 10

<210> 16
 <211> 33
 <212> DNA
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 <220>
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<400> 16
 agggccagtc agttcgttgg ctatagcatc cac 33

<210> 17
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<220>
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 <222> (8)..(8)
 <223> The residue in this position could be any amino acid

<400> 17

 Arg Ala Ser Gln Phe Val Gly Xaa Ser Ile His
 1 5 10

<210> 18
<211> 33
<212> DNA
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<220>
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<220>
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<222> (22)..(24)
<223> The residues in these positions could be any amino acid

<400> 18
agggccagtc agttcgttgg cnnnagcatc cac 33

<210> 19
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<220>
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<400> 19

Tyr Ala Ser Glu Ser Met Ser
1 5

<210> 20
<211> 21
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tatgcttctg agtctatgtc t 21

<210> 21
<211> 7
<212> PRT
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<220>
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<400> 21

Tyr Ala Ser Glu Tyr Met Ser
1 5

<210> 22
<211> 21
<212> DNA
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<220>
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<400> 22
tatgcttctg agtatatgtc t

21

<210> 23
<211> 7
<212> PRT
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<220>
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<220>
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<400> 23

Tyr Ala Ser Glu Xaa Met Ser
1 5

<210> 24
<211> 21
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<220>
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<220>
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<222> (13)..(15)
<223> The residues in these positions could be any amino acid

<400> 24
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21

<210> 25
<211> 7
<212> PRT
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<220>

<223> Synthetic Construct

<400> 25

Tyr Ala Ser Glu Ser Arg Ser
1 5

<210> 26

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 26

tatgcttctg agtctaggtc t

21

<210> 27

<211> 7

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 27

Tyr Ala Ser Glu Ser Lys Ser
1 5

<210> 28

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 28

tatgcttctg agtctaagtc t

21

<210> 29

<211> 7

<212> PRT

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<220>

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<222> (6)..(6)
<223> The residue in this position could be any amino acid

<400> 29

Tyr Ala Ser Glu Ser Xaa Ser
1 5

<210> 30
<211> 21
<212> DNA
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<220>
<223> Synthetic Construct

<220>
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<222> (16)..(18)
<223> The residues in these positions could be any amino acid

<400> 30
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<210> 31
<211> 7
<212> PRT
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<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (5)..(6)
<223> The residues in these positions could be any amino acid

<400> 31

Tyr Ala Ser Glu Xaa Xaa Ser
1 5

<210> 32
<211> 21
<212> DNA
<213> Artificial

<220>
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<221> misc_feature
<222> (13)..(18)
<223> The residues in these positions could be any amino acid

<400> 32
tatgcttctg agnnnnnntc t 21

<210> 33
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 33

Gln Gln Ser His Ser Trp His Phe Thr
1 5

<210> 34
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Synthetic Construct

<400> 34
caacaaagtc atagctggca tttcacg 27

<210> 35
<211> 10
<212> PRT
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<220>
<223> Synthetic Construct

<400> 35

Gly Phe Thr Phe Ser Asn His Trp Met Asn
1 5 10

<210> 36
<211> 30
<212> DNA
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<220>
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<400> 36

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30

<210> 37

<211> 10

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<213> Artificial

<220>

<223> Synthetic Construct

<400> 37

Gly Phe Lys Phe Ser Asn His Trp Met Asn
1 5 10

<210> 38

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 38

ggattcaagt tcagtaacca ctggatgaac

30

<210> 39

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 39

Gly Phe Pro Phe Ser Asn His Trp Met Asn
1 5 10

<210> 40

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 40

ggattccctt tcagtaacca ctggatgaac

30

<210> 41

<211> 10

<212> PRT
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<220>
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<220>
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<223> The residue in this position could be any amino acid

<400> 41

Gly Phe Xaa Phe Ser Asn His Trp Met Asn
1 5 10

<210> 42
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Synthetic Construct

<220>
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<222> (7)..(9)
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<400> 42
ggattcnnnt tcagtaacca ctggatgaac 30

<210> 43
<211> 19
<212> PRT
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<220>
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<400> 43

Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 44
<211> 57
<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 44

gaaattagat caaaatctat taattctgca acacattatg cggagtctgt gaaaggg 57

<210> 45

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 45

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 46

<211> 57

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 46

gaaattagat caaaatctat gaattctgca acacattatg cggagtctgt gaaaggg 57

<210> 47

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> The residue in this position could be any amino acid

<400> 47

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1 5 10 15

Val Lys Gly

<210> 48

<211> 57

<212> DNA

<213> Artificial

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<223> The residues in these positions could be any amino acid

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<210> 49

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 49

Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Arg Ser

1 5 10 15

Val Lys Gly

<210> 50

<211> 57

<212> DNA

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<220>

<223> Synthetic Construct

<400> 50

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<210> 51

<211> 19

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<222> (15)..(15)

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<400> 51

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1 5 10 15

Val Lys Gly

<210> 52

<211> 57

<212> DNA

<213> Artificial

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<220>

<221> misc_feature

<222> (43)..(45)

<223> The residues in these positions could be any amino acid

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<210> 53

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 53

Asn Tyr Tyr Gly Ser Thr Tyr Asp His
1 5

<210> 54

<211> 27

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 54

aattactacg gtagtaccta cgaccat

27

<210> 55

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 55

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Arg Ser
1 5 10 15

Val Lys Gly

<210> 56

<211> 57

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<400> 56

gaaattagat caaaatctat gaattctgca acacattatg cgcgttctgt gaaaggg

57